



FIG. 1

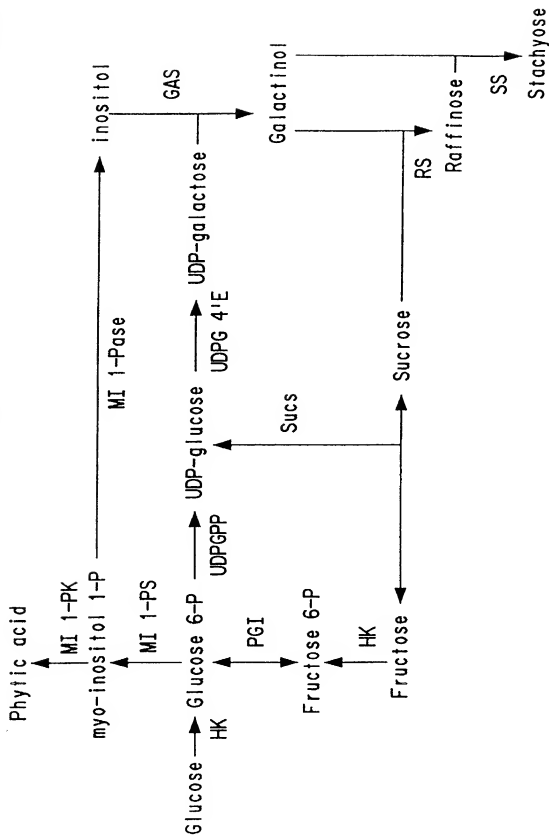


Figure 2

1
 SEQ ID NO:1 ATGTTCAATCGAGAAATTTTAAGGTGAGGTGCTCTAATGTGAAGTACACCGAGACTGAGATT
 SEQ ID NO:5 ATGTTCAATCGAGAAATTTTAAGGTGAGGTGCTCTAATGTGAAGTACACCGAGACTGAGATT
 SEQ ID NO:9 ATGTTCAATCGAGAAATTTTAAGGTGAGGTGCTCTAATGTGAAGTACACCGAGACTGAGATT
 SEQ ID NO:11 ATGTTCAATCGAGAAATTTTAAGGTGAGGTGCTCTAATGTGAAGTACACCGAGACTGAGATT
 SEQ ID NO:13 ATGTTCAATCGAGAAATTTTAAGGTGAGGTGCTCTAATGTGAAGTACACCGAGACTGAGATT
 SEQ ID NO:15 ATGTTCAATCGAGAAATTTTAAGGTGAGGTGCTCTAATGTGAAGTACACCGAGACTGAGATT

60
 61
 SEQ ID NO:1 CAGTCCGTGTACACTACGAAACACCGAACTTTGTTCAAGAGAACAGGAATGGCACCTAT
 SEQ ID NO:5 CAGTCCGTGTACACTACGAAACACCGAACTTTGTTCAAGAGAACAGGAATGGCACCTAT
 SEQ ID NO:9 CAGTCCGTGTACACTACGAAACACCGAACTTTGTTCAAGAGAACAGGAATGGCACCTAT
 SEQ ID NO:11 CAGTCCGTGTACACTACGAAACACCGAACTTTGTTCAAGAGAACAGGAATGGCACCTAT
 SEQ ID NO:13 CAGTCCGTGTACACTACGAAACACCGAACTTTGTTCAAGAGAACAGGAATGGCACCTAT
 SEQ ID NO:15 CAGTCCGTGTACACTACGAAACACCGAACTTTGTTCAAGAGAACAGGAATGGCACCTAT

120
 121
 SEQ ID NO:1 CAGTGGATTGTCAAACCCAAATCTGTCAATACGAATTTAAACCAACACATCCATGTGCT
 SEQ ID NO:5 CAGTGGATTGTCAAACCCAAATCTGTCAATACGAATTTAAACCAACACATCCATGTGCT
 SEQ ID NO:9 CAGTGGATTGTCAAACCCAAATCTGTCAATACGAATTTAAACCAACACATCCATGTGCT
 SEQ ID NO:11 CAGTGGATTGTCAAACCCAAATCTGTCAATACGAATTTAAACCAACACATCCATGTGCT
 SEQ ID NO:13 CAGTGGATTGTCAAACCCAAATCTGTCAATACGAATTTAAACCAACACATCCATGTGCT
 SEQ ID NO:15 CAGTGGATTGTCAAACCCAAATCTGTCAATACGAATTTAAACCAACACATCCATGTGCT

180
 181
 SEQ ID NO:1 AAATTAGGGGTAAATGCTTGTGGGTGGGGTGGAAACACGGCTCAACCTCAACGGTGGT
 SEQ ID NO:5 AAATTAGGGGTAAATGCTTGTGGGTGGGGTGGAAACACGGCTCAACCTCAACGGTGGT
 SEQ ID NO:9 AAATTAGGGGTAAATGCTTGTGGGTGGGGTGGAAACACGGCTCAACCTCAACGGTGGT
 SEQ ID NO:11 AAATTAGGGGTAAATGCTTGTGGGTGGGGTGGAAACACGGCTCAACCTCAACGGTGGT
 SEQ ID NO:13 AAATTAGGGGTAAATGCTTGTGGGTGGGGTGGAAACACGGCTCAACCTCAACGGTGGT
 SEQ ID NO:15 AAATTAGGGGTAAATGCTTGTGGGTGGGGTGGAAACACGGCTCAACCTCAACGGTGGT

240



10

241

Figure 2 (cont.)

481
 SEQ ID NO:1 ATCGATTTCGAGAGCAGTTGAGGCCCTTACATGGAATCCATGCTTCCACTCCCGGAAATC
 SEQ ID NO:5 ATCGATTTCGAGAGCAGTTGAGGCCCTTACATGGAATCCATGCTTCCACTCCCGGAAATC
 SEQ ID NO:9 ATCGATTTCGAGAGCAGTTGAGGCCCTTACATGGAATCCATGCTTCCACTCCCGGAAATC
 SEQ ID NO:11 ATCGATTTCGAGAGCAGTTGAGGCCCTTACATGGAATCCATGCTTCCACTCCCGGAAATC
 SEQ ID NO:13 ATCGATTTCGAGAGCAGTTGAGGCCCTTACATGGAATCCATGCTTCCACTCCCGGAAATC
 SEQ ID NO:15 ATCGATTTCGAGAGCAGTTGAGGCCCTTACATGGAATCCATGCTTCCACTCCCGGAAATC

541
 SEQ ID NO:1 TATACCCCGGATTTCAATTCGTCGAACCAAGAGGAGCGTGCCACACAGCTCATCAGGSGC
 SEQ ID NO:5 TATACCCCGGATTTCAATTCGTCGCCACACAGAGGAGCGGTGCCACACAGCTCATCAGGSGC
 SEQ ID NO:9 TATACCCCGGATTTCAATTCGTCGCCACACAGAGGAGCGGTGCCACACAGCTCATCAGGSGC
 SEQ ID NO:11 TATACCCCGGATTTCAATTCGTCGCCACACAGAGGAGCGGTGCCACACAGCTCATCAGGSGC
 SEQ ID NO:13 TATACCCCGGATTTCAATTCGTCGCCACACAGAGGAGCGGTGCCACACAGCTCATCAGGSGC
 SEQ ID NO:15 TATACCCCGGATTTCAATTCGTCGCCACACAGAGGAGCGGTGCCACACAGCTCATCAGGSGC

600
 SEQ ID NO:1 ACAACGACGAGCAGAGCTTCACAAATCATCAAGACATCAAGGCGTTTAAAGAGCCACCC
 SEQ ID NO:5 ACAACGACGAGCAGAGCTTCACAAATCATCAAGACATCAAGGCGTTTAAAGAGCCACCC
 SEQ ID NO:9 ACAACGACGAGCAGAGCTTCACAAATCATCAAGACATCAAGGCGTTTAAAGAGCCACCC
 SEQ ID NO:11 ACAACGACGAGCAGAGCTTCACAAATCATCAAGACATCAAGGCGTTTAAAGAGCCACCC
 SEQ ID NO:13 ACAACGACGAGCAGAGCTTCACAAATCATCAAGACATCAAGGCGTTTAAAGAGCCACCC
 SEQ ID NO:15 ACAACGACGAGCAGAGCTTCACAAATCATCAAGACATCAAGGCGTTTAAAGAGCCACCC

661
 SEQ ID NO:1 AAAGTGGACAAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTACAGTAATTTGGTT
 SEQ ID NO:5 AAAGTGGACAAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTACAGTAATTTGGTT
 SEQ ID NO:9 AAAGTGGACAAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTACAGTAATTTGGTT
 SEQ ID NO:11 AAAGTGGACAAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTACAGTAATTTGGTT
 SEQ ID NO:13 AAAGTGGACAAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTACAGTAATTTGGTT
 SEQ ID NO:15 AAAGTGGACAAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTACAGTAATTTGGTT

720
 SEQ ID NO:1 AAAGTGGACAAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTACAGTAATTTGGTT
 SEQ ID NO:5 AAAGTGGACAAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTACAGTAATTTGGTT
 SEQ ID NO:9 AAAGTGGACAAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTACAGTAATTTGGTT
 SEQ ID NO:11 AAAGTGGACAAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTACAGTAATTTGGTT
 SEQ ID NO:13 AAAGTGGACAAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTACAGTAATTTGGTT
 SEQ ID NO:15 AAAGTGGACAAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTACAGTAATTTGGTT

Figure 2 (cont.)

721
 SEQ ID NO:1 GTGGGCTTAATGACACCATGGAGAATCTCTTGGCTGCTGTGGACAGAAATGAGGCTGAG
 SEQ ID NO:5 GTGGGCTTAATGACACCATGGAGAATCTCTTGGCTGCTGTGGACAGAAATGAGGCTGAG
 SEQ ID NO:9 GTGGGCTTAATGACACCATGGAGAATCTCTTGGCTGCTGTGGACAGAAATGAGGCTGAG
 SEQ ID NO:11 GTGGGCTTAATGACACCATGGAGAATCTCTTGGCTGCTGTGGACAGAAATGAGGCTGAG
 SEQ ID NO:13 GTGGGCTTAATGACACCATGGAGAATCTCTTGGCTGCTGTGGACAGAAATGAGGCTGAG
 SEQ ID NO:15 GTGGGCTTAATGACACCATGGAGAATCTCTTGGCTGCTGTGGACAGAAATGAGGCTGAG

780
 781
 SEQ ID NO:1 ATTTCTCCTTCACCTTGATGCCATTGCTGTGTATGAAAAATGTTCTTCATTAAAT
 SEQ ID NO:5 ATTTCTCCTTCACCTTGATGCCATTGCTGTGTATGAAAAATGTTCTTCATTAAAT
 SEQ ID NO:9 ATTTCTCCTTCACCTTGATGCCATTGCTGTGTATGAAAAATGTTCTTCATTAAAT
 SEQ ID NO:11 ATTTCTCCTTCACCTTGATGCCATTGCTGTGTATGAAAAATGTTCTTCATTAAAT
 SEQ ID NO:13 ATTTCTCCTTCACCTTGATGCCATTGCTGTGTATGAAAAATGTTCTTCATTAAAT
 SEQ ID NO:15 ATTTCTCCTTCACCTTGATGCCATTGCTGTGTATGAAAAATGTTCTTCATTAAAT

841
 SEQ ID NO:1 GGAAGCCCTCAGAACACTTTTGTACAGGGCTGATTGATCTTGCCATCGCAGGAACACT
 SEQ ID NO:5 GGAAGCCCTCAGAACACTTTTGTACAGGGCTGATTGATCTTGCCATCGCAGGAACACT
 SEQ ID NO:9 GGAAGCCCTCAGAACACTTTTGTACAGGGCTGATTGATCTTGCCATCGCAGGAACACT
 SEQ ID NO:11 GGAAGCCCTCAGAACACTTTTGTACAGGGCTGATTGATCTTGCCATCGCAGGAACACT
 SEQ ID NO:13 GGAAGCCCTCAGAACACTTTTGTACAGGGCTGATTGATCTTGCCATCGCAGGAACACT
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901
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 SEQ ID NO:13 TTGATTGGTGAGATGACTTCAAGAGTGGTCAGACCAAAAATGAAAATCTGTGTGGTTGAT
 SEQ ID NO:15 TTGATTGGTGAGATGACTTCAAGAGTGGTCAGACCAAAAATGAAAATCTGTGTGGTTGAT

961
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 SEQ ID NO:5 TTCTTTGGGGGCTGGTATCAAGCAACATCTATAGTCAGTTACAACCATCTGGGAAC
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 SEQ ID NO:13 TTCTTTGGGGGCTGGTATCAAGCAACATCTATAGTCAGTTACAACCATCTGGGAAC
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1021
 1021
 SEQ ID NO:1 TTCTTTGGGGGCTGGTATCAAGCAACATCTATAGTCAGTTACAACCATCTGGGAAC
 SEQ ID NO:5 TTCTTTGGGGGCTGGTATCAAGCAACATCTATAGTCAGTTACAACCATCTGGGAAC
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 SEQ ID NO:13 TTCTTTGGGGGCTGGTATCAAGCAACATCTATAGTCAGTTACAACCATCTGGGAAC
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Figure 2 (cont..)

1261
 SEQ ID NO:1 GAGGATTCCTCTTACGTGCTCCTATATCTTGAGACTTGGTCTCTTCTGAGCTGAGC.
 SEQ ID NO:5 GAGGATTCCTCTTACGTGCTCCTATATCTTGAGACTTGGTCTCTTCTGAGCTGAGC.
 SEQ ID NO:9 GAGGATTCCTCTTACGTGCTCCTATATCTTGAGACTTGGTCTCTTCTGAGCTGAGC.
 SEQ ID NO:11 GAGGATTCCTCTTACGTGCTCCTATATCTTGAGACTTGGTCTCTTCTGAGCTGAGC.
 SEQ ID NO:13 GAGGATTCCTCTTACGTGCTCCTATATCTTGAGACTTGGTCTCTTCTGAGCTGAGC.
 SEQ ID NO:15 GAGGATTCCTCTTACGTGCTCCTATATCTTGAGACTTGGTCTCTTCTGAGCTGAGC.

1321
 SEQ ID NO:1 ACTAGATCCAGTTTAAAGCTGAAATGAGGAAATTCACACTCAITTCACCCAGTTGCT
 SEQ ID NO:5 ACTAGATCCAGTTTAAAGCTGAAATGAGGAAATTCACACTCAITTCACCCAGTTGCT
 SEQ ID NO:9 ACTAGATCCAGTTTAAAGCTGAAATGAGGAAATTCACACTCAITTCACCCAGTTGCT
 SEQ ID NO:11 ACTAGATCCAGTTTAAAGCTGAAATGAGGAAATTCACACTCAITTCACCCAGTTGCT
 SEQ ID NO:13 ACTAGATCCAGTTTAAAGCTGAAATGAGGAAATTCACACTCAITTCACCCAGTTGCT
 SEQ ID NO:15 ACTAGATCCAGTTTAAAGCTGAAATGAGGAAATTCACACTCAITTCACCCAGTTGCT

1381
 SEQ ID NO:1 ACCATCTCAGCTACTCCACAGGCTCCTCTGGTTCCACCGGATACACAGTGGTGAAT
 SEQ ID NO:5 ACCATCTCAGCTACTCCACAGGCTCCTCTGGTTCCACCGGATACACAGTGGTGAAT
 SEQ ID NO:9 ACCATCTCAGCTACTCCACAGGCTCCTCTGGTTCCACCGGATACACAGTGGTGAAT
 SEQ ID NO:11 ACCATCTCAGCTACTCCACAGGCTCCTCTGGTTCCACCGGATACACAGTGGTGAAT
 SEQ ID NO:13 ACCATCTCAGCTACTCCACAGGCTCCTCTGGTTCCACCGGATACACAGTGGTGAAT
 SEQ ID NO:15 ACCATCTCAGCTACTCCACAGGCTCCTCTGGTTCCACCGGATACACAGTGGTGAAT

1441
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 SEQ ID NO:5 GCATTGTCAAAGCAGCGTCAATGCTGGAAACATAATGAGGCTTGTGTTGATTGSCC
 SEQ ID NO:9 GCATTGTCAAAGCAGCGTCAATGCTGGAAACATAATGAGGCTTGTGTTGATTGSCC
 SEQ ID NO:11 GCATTGTCAAAGCAGCGTCAATGCTGGAAACATAATGAGGCTTGTGTTGATTGSCC
 SEQ ID NO:13 GCATTGTCAAAGCAGCGTCAATGCTGGAAACATAATGAGGCTTGTGTTGATTGSCC
 SEQ ID NO:15 GCATTGTCAAAGCAGCGTCAATGCTGGAAACATAATGAGGCTTGTGTTGATTGSCC

1501
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 SEQ ID NO:5 CCAGAGAATAACATGATTCTCGAGTACAAGTGA
 SEQ ID NO:9 CCAGAGAATAACATGATTCTCGAGTACAAGTGA
 SEQ ID NO:11 CCAGAGAATAACATGATTCTCGAGTACAAGTGA
 SEQ ID NO:13 CCAGAGAATAACATGATTCTCGAGTACAAGTGA
 SEQ ID NO:15 CCAGAGAATAACATGATTCTCGAGTACAAGTGA

1533
 SEQ ID NO:1 CCAGAGAATAACATGATTCTCGAGTACAAGTGA
 SEQ ID NO:5 CCAGAGAATAACATGATTCTCGAGTACAAGTGA
 SEQ ID NO:9 CCAGAGAATAACATGATTCTCGAGTACAAGTGA
 SEQ ID NO:11 CCAGAGAATAACATGATTCTCGAGTACAAGTGA
 SEQ ID NO:13 CCAGAGAATAACATGATTCTCGAGTACAAGTGA
 SEQ ID NO:15 CCAGAGAATAACATGATTCTCGAGTACAAGTGA

Figure 3

1
 SEQ ID NO:2
 SEQ ID NO:6
 SEQ ID NO:10
 SEQ ID NO:12
 SEQ ID NO:14
 SEQ ID NO:16
 MIENFKVCSNWKYTEIQSYVNYETTELHENRNGTYQWIVKPSVKFEKTNTHVP
 MIENFKVCSNWKYTEIQSYVNYETTELHENRNGTYQWIVKPSVKFEKTNTHVP
 MIENFKVCSNWKYTEIQSYVNYETTELHENRNGTYQWIVKPSVKFEKTNTHVP
 MIENFKVCSNWKYTEIQSYVNYETTELHENRNGTYQWIVKPSVKFEKTNTHVP
 MIENFKVCSNWKYTEIQSYVNYETTELHENRNGTYQWIVKPSVKFEKTNTHVP
 MIENFKVCSNWKYTEIQSYVNYETTELHENRNGTYQWIVKPSVKFEKTNTHVP
 60
 61
 SEQ ID NO:2
 SEQ ID NO:6
 SEQ ID NO:10
 SEQ ID NO:12
 SEQ ID NO:14
 SEQ ID NO:16
 KLGVLVGVGGNGNSTLGGVIANREGISWATKDKIQOANVFGSLTQASAIRVGSFQSEE
 KLGVLVGVGGNGNSTLGGVIANREGISWATKDKIQOANVFGSLTQASAIRVGSFQSEE
 KLGVLVGVGGNGNSTLGGVIANREGISWATKDKIQOANVFGSLTQASAIRVGSFQSEE
 KLGVLVGVGGNGNSTLGGVIANREGISWATKDKIQOANVFGSLTQASAIRVGSFQSEE
 KLGVLVGVGGNGNSTLGGVIANREGISWATKDKIQOANVFGSLTQASAIRVGSFQSEE
 KLGVLVGVGGNGNSTLGGVIANREGISWATKDKIQOANVFGSLTQASAIRVGSFQSEE
 120
 121
 SEQ ID NO:2
 SEQ ID NO:6
 SEQ ID NO:10
 SEQ ID NO:12
 SEQ ID NO:14
 SEQ ID NO:16
 IYAFKSKLLPMVNPDDIVFGGWDISNNLADAMARAKVFDIDLOKLREYMESMLPLPGI
 IYAFKSKLLPMVNPDDIVFGGWDISNNLADAMARAKVFDIDLOKLREYMESMLPLPGI
 IYAFKSKLLPMVNPDDIVFGGWDISNNLADAMARAKVFDIDLOKLREYMESMLPLPGI
 IYAFKSKLLPMVNPDDIVFGGWDISNNLADAMARAKVFDIDLOKLREYMESMLPLPGI
 IYAFKSKLLPMVNPDDIVFGGWDISNNLADAMARAKVFDIDLOKLREYMESMLPLPGI
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 180
 181
 SEQ ID NO:2
 SEQ ID NO:6
 SEQ ID NO:10
 SEQ ID NO:12
 SEQ ID NO:14
 SEQ ID NO:16
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 YPDPFTAAHQEERANNVIGTKQEQQVQIIKOIKAFKEATKVDKVVVLWTANTERYSNLV
 YPDPFTAAHQEERANNVIGTKQEQQVQIIKOIKAFKEATKVDKVVVLWTANTERYSNLV
 YPDPFTAAHQEERANNVIGTKQEQQVQIIKOIKAFKEATKVDKVVVLWTANTERYSNLV
 YPDPFTAAHQEERANNVIGTKQEQQVQIIKOIKAFKEATKVDKVVVLWTANTERYSNLV
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 240

Figure 3 (cont.)

241
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 SEQ ID NO:6 VGLNDTWNLLAADVDRNEAEISPSLVAIAACWENVFINGSPONTFVPGILDIAIARNT
 SEQ ID NO:10 VGLNDTWNLLAADVDRNEAEISPSLVAIAACWENVFINGSPONTFVPGILDIAIARNT
 SEQ ID NO:12 VGLNDTWNLLAADVDRNEAEISPSLVAIAACWENVFINGSPONTFVPGILDIAIARNT
 SEQ ID NO:14 VGLNDTWNLLAADVDRNEAEISPSLVAIAACWENVFINGSPONTFVPGILDIAIARNT
 SEQ ID NO:16 VGLNDTWNLLAADVDRNEAEISPSLVAIAACWENVFINGSPONTFVPGILDIAIARNT

301
 SEQ ID NO:2 LIGGDDFKSGQTRKMSVLVDFLVGAGIKPTSVSYNHLGNNDGNNLSAPOTFRSKEISKS 360
 SEQ ID NO:6 LIGGDDFKSGQTRKMSVLVDFLVGAGIKPTSVSYNHLGNNDGNNLSAPOTFRSKEISKS
 SEQ ID NO:10 LIGGDDFKSGQTRKMSVLVDFLVGAGIKPTSVSYNHLGNNDGNNLSAPOTFRSKEISKS
 SEQ ID NO:12 LIGGDDFKSGQTRKMSVLVDFLVGAGIKPTSVSYNHLGNNDGNNLSAPOTFRSKEISKS
 SEQ ID NO:14 LIGGDDFKSGQTRKMSVLVDFLVGAGIKPTSVSYNHLGNNDGNNLSAPOTFRSKEISKS
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361
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 SEQ ID NO:6 NVDDWVNSNALLYERGEHPDHVVVVKYVPYVGDSCRAMDEYTSIEFMGGKSTIVLHNTC
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 SEQ ID NO:12 NVDDWVNSNALLYERGEHPDHVVVVKYVPYVGDSCRAMDEYTSIEFMGGKSTIVLHNTC
 SEQ ID NO:14 NVDDWVNSNALLYERGEHPDHVVVVKYVPYVGDSCRAMDEYTSIEFMGGKSTIVLHNTC
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421
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 SEQ ID NO:12 EDSLAAAPITILDVLLAELSTRLEFKAENEGKFSFHPVATILSYLTAKPLVPPGTPVWN
 SEQ ID NO:14 EDSLAAAPITILDVLLAELSTRLEFKAENEGKFSFHPVATILSYLTAKPLVPPGTPVWN
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481
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 SEQ ID NO:14 ALSKQRAMLENIMRACVGLAPENNNMILEYK
 SEQ ID NO:16 ALSKQRAMLENIMRACVGLAPENNNMILEYK